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a computing device receiving the data set and performing the steps of:

- generating corrected data by processing the data set to remove noise due to system and chemical reaction characteristics, the corrected data set having putative peak areas;
- using the putative peaks to remove residual baseline effects;
- defining the position of expected peaks using known possible peak areas from the biological sample;
- shifting the corrected data set to more closely align the putative peaks to the expected peaks;
- calculating the probability that the putative peaks in the shifted data set are actual peaks; and
- calling the composition of the biological sample responsive to the calculated probability, to thereby identify a component in the sample.

REMARKS

A check for the fees for a one-month extension of time accompanies this response. Any fees that may be due in connection with this application throughout its pendency may be charged to Deposit Account No. 50-1213.

Claims 1-45 are presently pending in this application. Claims 1, 12, 13, 19, 20-21, 38, and 40-45 are amended herein to more distinctly claim the subject matter claimed by the applicant.

In compliance with our duty of disclosure, the Examiner's attention is directed to co-pending U.S. application Serial No. 09/285,481, filed April 2, 1999, by Köster *et al.* Commonly-owned U.S. application Serial No. 09/285,481 ('481) is directed to systems and methods for high throughput processing of biological samples. It is noted that no rejections for obviousness-type double patenting are pending. If such rejection is made, the Office is

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Claim 1 is amended to replace the recitation "data set indicative of the composition of the biological sample" with the recitation —data set comprising compositional data regarding the biological sample— to more distinctly claim the subject matter by removing the phrase "indicative of" objected to by the Examiner. Claims 1, 38, and 40 are amended to replace the recitation "deleting the baseline" with the recitation —correcting the baseline— to more distinctly claim the subject matter. Basis is found on page 8, lines 14-24.

Claims 1, 38, 40, 41, and 45 are amended to replace the recitation "using the putative peaks to generate a residual baseline" with the recitation —using the putative peaks to remove residual baseline effects, generating a residual baseline— to more distinctly claim the subject matter. Basis is found throughout the specification (for example, page 18, lines 1-20).

Claims 1 and 38 are amended to delete the recitation "responsive to removing the residual baseline" to improve the grammar of the claim and to remove any ambiguity. Claim 12 is amended to correct dependency, as claim 12 properly depends from claim 11, and not claim 7 as previously indicated. Claim 13 is amended to replace the recitation "indicative of" with the recitation —comprising— to more distinctly claim the subject matter, and basis for the amendment can be found on page 13, lines 20-21.

Claim 19 is amended to more distinctly claim the subject matter of compressing the intermediate data set, basis for which is found in the specification (for example, see page 16, lines 17-29, and FIG. 19). Claims 20 and 21 are amended to more distinctly claim the subject matter of the compressed data value, basis for which is found in the specification (for example, see page 15, lines 23-30).

Claim 43 is amended to correct dependency, and to more distinctly claim the subject matter. Basis for the amendment is found throughout the

specification (for example, see page 16, lines 17-29). Claim 44 is amended to correct

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dependency and to more to more distinctly claim the subject matter. Basis for the amendment can be found throughout the specification (see page 20, lines 23-28). Claim 45 is amended to more to more distinctly claim the subject matter, by including the recitation —to thereby identify a compound in the sample— in order to make the final process step agree back to the preamble.

No new matter is added nor are any amendments made to change the scope of the claims. The amendments should place the claims and the application into condition for allowance.

Included as an attachment is a marked-up version of the claims that are being amended, as per 37 CFR §1.121.

Formal drawings were submitted to the Drawing Review Branch under separate cover on September 10, 2002.

REJECTION OF CLAIMS 1-21 UNDER 35 U.S.C. § 112, SECOND PARAGRAPH

Claims 1-45 are rejected under 35 U.S.C. § 112, second paragraph, for allegedly being indefinite due to the lack of claim language and thus failing to clearly claim the subject matter.

This rejection is respectfully traversed.

RELEVANT LAW

Claims are not read in a vacuum but instead are considered in light of the specification and the general understanding of the skilled artisan. Rosemount Inc. v. Beckman Instruments, Inc., 727 F.2d 1540, 1547, 221 USPQ 1, 7 (Fed. Cir. 1984), Caterpillar Tractor Co. v. Berco, S.P.A., 714 F.2d 1110, 1116, 219 USPQ 185, 188 (Fed. Cir. 1983). A claim is not indefinite when one skilled in the art would understand the language in the claims when read in light of the specification.

35 U.S.C. § 112, second paragraph requires only reasonable precision in defining the claimed subject matter so that those of skill in the art can reasonably apprise those of skill in the art of the bounds of the claimed

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invention and is as precise as the subject matter permits. Shatterproof Glass Corp. v. Libby-Owens Ford Col., 758 F.2d 613, 624, 225 USPQ 634, 641 (Fed. Cir.), cert. dismissed, 106 S.Ct. 340 (1985).

ANALYSIS

Claims 1 and 13

The Examiner alleges that the use of the recitation "data set indicative of the composition" in claim 1 and "sparse data set indicative of the denoised data" in claim 13 is vague and indefinite, and suggests that the issue can be resolved by particularly pointing to the criteria/range/value by which the data set is indicative of the composition or the denoised data.

It is respectfully submitted that these objections are obviated by amendment of claims 1 and 13 herein. Applicant respectfully requests that the rejection be withdrawn.

Claims 1, 38, and 40

The Examiner alleges that the use of the recitation "responsive to removing the residual baseline" in claims 1, 38, and 40 is vague and indefinite.

It is respectfully submitted that these objections are obviated by amendment of claims 1, 38, and 40 herein. Applicant respectfully requests that the rejection be withdrawn.

Claims 6 and 8

The Examiner alleges that the use of the recitation "stage 0" in claims 6 and 8 is vague and indefinite because it is unclear what "stage 0" represents. The specification teaches on page 8, lines 8-10 that

[i]n using wavelets, a "small wave" or "scaling function" is used to transform a data set into stages, with each stage representing a frequency component in the data set.

on page 10, line 19 through page 11, line 1, the specification teaches.

Referring now to FIG. 4, the wavelet transformation of the raw mass spectrometry data is generally diagramed. Using wavelet transformation techniques, the mass spectrometry data 70 is sequentially transformed into stages. In each stage the data is represented in a high stage and a low stage, with the low stage acting as the input to the next sequential stage. For example, the mass spectrometry data 70 is transformed into stage 0 high data 82 and stage 0 low data 83. The stage 0 low data 83 is then used as an input to the next level transformation to generate stage 1 high data 84 and stage 1 low data 85. In a similar manner, the stage 1 low data 85 is used as an input to be transformed into stage 2 high data 86 and stage 2 low data 87. The transformation is continued until no more useful information can be derived by further wavelet transformation.

Thus, stage 0 refers to the first wavelet transformed data set. Therefore, when read in light of the specification, one skilled in the art would understand the language in the claims, and claims 6 and 8 are not indefinite. Applicant respectfully requests that the rejection be withdrawn.

Claims 19-21

The Examiner alleges that the use of the recitation "compressing the intermediate data set" in claim 19 is confusing because it is unclear when the intermediate data set is compressed, and further contends that there is no indication of a compressed intermediate data set in claim 1. The Examiner further alleges that the use of the recitation "compressed data value" is vague and indefinite because applicant fails to indicate the purpose/use of "compressed data value" to the instantly claimed "invention".

It is respectfully submitted that these objections are obviated by amendment of claims 19-21 herein. Applicant respectfully requests that the objections be withdrawn.

Claim 45

The Examiner alleges that claim 45 is indefinite due to the lack of clarity in the claim language. The Examiner alleges that the claim language is inconsistent with the preamble. The Examiner alleges that the preamble states that it is a

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"system for identifying a component in a biological sample" but contends that the final step does not indicate that a component in a biological sample is to be identified.

It is respectfully submitted that this objection is obviated by amendment of claim 45 herein. Applicant respectfully requests that the objection be withdrawn.

Claims 12, 15, and 44

Claims 12, 15, and 44 are objected to as allegedly containing recitations which lack clear antecedent basis. These objections are obviated by the amendment to the claims made herein. Applicant respectfully requests that the objections be withdrawn.

THE REJECTION OF CLAIMS 1-4, 15-18, 38-41 AND 45 UNDER 35 U.S.C. §102(b)

Claims 1-4, 15-18, 38-41 and 45 are rejected under 35 U.S.C. § 102(b) as anticipated by Green *et al.* (US 5,853,979) because Green *et al.* allegedly discloses a method and system to normalize experimental fragment patterns for nucleic acid polymers where a raw fragment pattern is conditioned using conventional baseline correction and noise reduction techniques to produce a produce a clean fragment pattern, and discloses that the method can be implemented using a computer, thus allegedly disclosing all aspects of the instantly claimed subject matter.

This rejection is respectfully traversed.

RELEVANT LAW

Anticipation requires the disclosure in a single prior art reference of each element of the claim under consideration. In re Spada, 15 USPQ2d 1655 (Fed. Cir, 1990), In re Bond, 15 USPQ 1566 (Fed. Cir. 1990), Soundsciber Corp. v. U.S., 360 F.2d 954, 148 USPQ 298, 301, adopted 149 USPQ 640 (Ct. Cl.)

USPQ2d 1913, 1920 (Fed. Cir. 1990) cert. denied 494 U.S. 1091 (1990).

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limitations in the claims must be found in the reference, since the claims measure the invention". In re Lang, 644 F.2d 856, 862, 209 USPQ 288, 293 (CCPA 1981). Moreover it is incumbent on Examiner to identify wherein each and every facet of the claimed invention is disclosed in the reference. Lindemann Maschinen-fabrik GmbH v. American Hoist and Derrick Co., 730 F.2d 1452, 221 USPQ 481 (Fed. Cir. 1984). Further, the reference must describe the invention as claimed sufficiently to have placed a person of ordinary skill in the art in possession of the invention. An inherent property has to flow naturally from what is taught in a reference In re Oelrich, 666 F.2d 578, 581, 212 USPQ 323, 326 (CCPA 1981).

THE CLAIMS

Claim 1 is directed to a method for identifying a biological sample, which includes generating a data set including compositional data regarding the biological sample; denoising the data set to generate denoised data; correcting the baseline from the denoised data to generate an intermediate data set; defining putative peaks for the biological sample; using the putative peaks to remove residual baseline effects, generating a residual baseline; removing the residual baseline from the intermediate data set to generate a corrected data set; locating a probable peak in the corrected data set; and identifying, using the located probable peak, the biological sample.

Claim 38 is directed to a system for identifying a biological sample, the system including an instrument receiving the biological sample and generating a data set indicative of the composition of the biological sample; a computer communicating to the instrument and configured to receive the generated data set, where the computer denoises the data set to generate denoised data, corrects the baseline from the denoised data to generate an intermediate data set; defines putative peaks for the biological sample; uses the putative peaks to remove residual baseline effects, generating a residual baseline; removing the residual baseline from the intermediate data set to generate a corrected data set;

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locates a probable peak in the corrected data set; and identifies the biological sample using the located probable peak.

Claim 40 is directed to a machine readable program operating on a computing device, where the computing device is configured to receive a data set indicating composition of a biological sample, where the program implements the steps of denoising the data set to generate denoised data; deleting the baseline from the denoised data to generate an intermediate data set; defining putative peaks for the biological sample; using the putative peaks to remove residual baseline effects, generating a residual baseline; removing the residual baseline from the intermediate data set to generate a corrected data set; locating a probable peak in the corrected data set; and identifying, using the located probable peak, the biological sample.

Claim 41 is directed to a system for identifying a component of a DNA sample, including a mass spectrometer receiving the DNA sample and generating a data set indicative of the composition of the DNA sample; a computing device configured to receive the data set, the computing device implementing the method including denoising the data set to generate denoised data; correcting the baseline from the denoised data to generate a corrected data set having putative peaks; using the putative peaks to remove residual baseline effects; locating a probable peak in the corrected data set; and identifying, using the located probable peak, a component in the composition of the DNA sample.

Claim 45 is directed to a system for identifying a component in a biological sample, including an instrument receiving the biological sample and generating a data set indicative of the component in the biological sample; a computing device receiving the data set and performing the steps of generating corrected data by processing the data set to remove noise due to system and chemical reaction characteristics, the corrected data set having putative peak areas; using the

expected peaks using known possible peak areas from the biological sample; shifting the corrected data set to more closely align the putative peaks to the

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expected peaks; calculating the probability that the putative peaks in the shifted data set are actual peaks; identifying the composition of the biological sample responsive to the calculated probability.

Disclosure of Green *et al.*

Green *et al.* discloses a method and system for normalization of experimental fragment patterns for nucleic acid polymers having putatively known sequences, where at least one raw fragment pattern is obtained for the experimental sample, the sample is conditioned using conventional baseline correction and noise reduction techniques, and the resulting clean fragment pattern is evaluated to determine one or more normalization coefficients which reflect the displacement, stretching or shrinking, and rate of stretching or shrinking of the clean fragment necessary to produce a high degree of correlation between the clean fragment pattern and a standard fragment pattern, the normalization coefficients then being used to produce a normalized fragment pattern which is used for base-calling in a conventional manner (col. 3, lines 42-64). The method can be implemented in an apparatus including a computer processor programmed to determine normalization coefficients for an experimental fragment pattern (col. 4, lines 10-15). Green *et al.* discloses conditioning the sample using conventional baseline correction and noise reduction techniques, using background subtraction, low frequency filtration, or high frequency filtration, or any combination thereof (col. 5, lines 19-49). The reference discloses generation of a standard fragment pattern to be used in determining the normalization coefficients for correcting the experimental data (col. 5, line 60 through col. 6, line 43).

Differences between the claimed subject matter and the disclosure of the Green *et al.*

Each of independent claims 1, 38, 40, 41, and 45 includes using the

disclose baseline removal from the sample data that includes the step of using putative peaks to remove residual baseline effects. Green *et al.* discloses using

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background subtraction, low frequency filtration, or high frequency filtration as methods of signal processing for baseline correction and noise reduction. Green *et al.* does not disclose defining the putative peaks by comparing them to known locations of expected peaks to determine the probability that each putative peak in the data is an actual peak, and using the putative peaks to remove residual baseline effects, generating a residual baseline. Instead, Green *et al.* discloses that the experimental sample is conditioned using conventional baseline correction and noise reduction techniques, and then the resulting clean fragment pattern is compared to a putative standard fragment pattern to determine normalization coefficients which reflect the displacement, stretching or shrinking, and rate of stretching or shrinking of the clean fragment to produce a high degree of correlation between the clean fragment pattern and a standard fragment pattern (col. 3, lines 42-60). Hence, Green *et al.* discloses that the experimental data is conditioned prior to comparison to putative peaks, and does not disclose using the putative peaks to remove residual baseline effects from the experimental data.

Thus, because Green *et al.* does not disclose every element of the claimed subject matter, this reference does not anticipate the claimed subject matter. Therefore, because Green *et al.* does not disclose all elements of the claimed subject matter in independent claims 1, 38, 40, 41, and 45, Green *et al.* does not anticipate any of the pending claims.

REJECTION OF CLAIMS 1-12, 15-21, 27, 28, 38-41, and 45 UNDER 35 U.S.C. §103(a)

Claims 1-12, 15-21, 27, 28, 38-41, and 45 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Green *et al.* in view of Cai *et al.* (*J. Chem Inf. Comput. Sci.* 38: 1161-70 (1998)) because Green *et al.* allegedly teaches or suggests a method and system to normalize experimental fragment patterns for

except the utilization of wavelet transformation to denoise the data. Cai *et al.* allegedly cures this defect. The Examiner contends that one of ordinary skill

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in the art would be motivated to utilize wavelet transformations taught by Cai *et al.* in combination with the methods of Green *et al.* to further reduce noise from experimental fragment patterns because Cai *et al.* states that experimental measurements contain interfering noise which limits the interpretation of data.

Relevant Law

In order to set forth a *prima facie* case of obviousness under 35 U.S.C. §103: (1) there must be some teaching, suggestion or incentive supporting the combination of cited references to produce the claimed invention (ACS Hospital Systems, Inc. v. Montefiore Hospital, 732 F.2d 1572, 1577, 221 USPQ 329, 933 (Fed. Cir. 1984)) and (2) the combination of the cited references must actually teach or suggest the claimed invention. Further, that which is within the capabilities of one skilled in the art is not synonymous with that which is obvious. Ex parte Gerlach, 212 USPQ 471 (Bd. APP. 1980). Obviousness is tested by "what the combined teachings of the references would suggest to those of ordinary skill in the art" In re Keller, 642 F.2d 413, 425, 208 USPQ 871, 881 (CCPA 1981), but it cannot be established by combining the teachings of the prior art to produce the claimed invention, absent some teaching or suggestion supporting the combination (ACS Hosp. Systems, Inc. v Montefiore Hosp. 732 F.2d 1572, 1577. 221 USPQ 329, 933 (Fed. Cir. 1984)).

"To imbue one of ordinary skill in the art with knowledge of the invention in suit, when no prior art reference or references of record convey or suggest that knowledge, is to fall victim to the insidious effect of a hindsight syndrome wherein that which only the inventor taught is used against its teacher" W.L. Gore & Associates, Inc. v. Garlock Inc., 721 F.2d 1540, 1553, 220 USPQ 303, 312-13 (Fed. Cir. 1983).

THE CLAIMS

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Differences Between the Claims and the Teachings of the Cited References

Green *et al.*

See related section above (page 13).

Cai *et al.*

Cai *et al.* teaches different wavelet transforms and their application for data compression, fast computation, and noise reduction of analytical data. Cai *et al.* teaches that there are about 22 wavelet types and that selecting the best wavelet type for specific data is difficult (page 1162, col. 2, lines 29-30), and that correct wavelet filter selection is essential to achieve the advantages of wavelet transformation over standard Fourier compression (page 1169, col. 1, lines 17-22). Cai *et al.* teaches that improper wavelet filter selection may result in problems in denoising the data (page 1168, col. 2, last paragraph). Cai *et al.* teaches that proper selection of the filter and thresholding can result in denoised data with the least RMS errors (page 1163, col. 2, last paragraph).

Cai *et al.* does not teach or suggest any post-denoising modifications or methods for removing residual baseline effects after denoising the data. Cai *et al.* does not teach or suggest identifying a putative peak and using the putative peak to remove residual baseline effects subsequent to denoising the data.

ANALYSIS

It is respectfully submitted that the Examiner has failed to set forth a case of *prima facie* obviousness for the following reasons.

The combination of teachings of Green *et al.* with the teachings of Cai *et al.* does not result in the instantly claimed systems.

As discussed in the traverse of the rejection under 35 U.S.C. § 102(b), Green *et al.* does not teach or suggest using putative peaks to remove residual baseline effects from the experimental data. Cai *et al.* does not cure this defect. Cai *et al.* teaches that wavelet transforms for denoising data includes three steps

First, data objects are transformed into the wavelet domain. Second, some coefficients are selected and

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zero-filled or "shrunk" by some criterion. Third, the shrunk coefficients are inversely transformed to the original domain, which is the denoised data.

Cai *et al.* teaches that the second step, determining a threshold and the treatment of wavelet coefficients that are below this threshold, is the most important step (page 1162, col. 2, lines 19-25). Cai *et al.* teaches that wavelet transforms are a means to compress measurement data and to remove unwanted noise (page 1169, col. 1, first full paragraph). Cai *et al.* does not teach or suggest identifying a putative peak and using the putative peak to remove residual baseline effects after denoising the data. In fact, Cai *et al.* does not teach or suggest any post-denoising methods or modifications for removing residual baseline effects after denoising the data. Cai *et al.* teaches only the application of wavelet transformation to denoising data, and evaluates different wavelet transform methods and threshold criteria. There is no suggestion or teaching of removing additional noise subsequent to denoising the data.

Combining the teachings of Green *et al.* with the teachings of Cai *et al.* does not result in methods or systems that remove additional noise from the data subsequent to denoising the data. Neither Green *et al.* nor Cai *et al.*, singly or in combination, teaches or suggests any post-denoising methods or modifications for removing residual baseline effects after denoising the data. Both Green *et al.* (col. 5, lines 19-24) and Cai *et al.* (page 1161, col. 1, first paragraph) teach or suggest that conventional baseline correction and noise reduction techniques remove noise from the baseline. There is no teaching or suggestion in Green *et al.* or Cai *et al.* of identifying a putative peak and using the putative peak to remove residual baseline effects subsequent to denoising the data.

Thus, the combination of the teachings of Green *et al.* with the teachings of Cai *et al.* does not result in the subject matter of the instant claims.

Therefore, because the combination of teachings of the references does not form a *prima facie* case of obviousness.

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OBJECTION OF CLAIM 2 UNDER 37 C.F.R. §1.75

The Examiner objects to claim 2 under 37 C.F.R. §1.75 as being a substantial duplicate of claim 3, alleging that claim 2 and claim 3 are directed to a spectrometry data set. Applicant respectfully disagrees. Claim 2 is directed to the method of claim 1, where the data set is a spectrometry data set. Claim 3 is directed to the method of claim 1, where the data set is generated by a mass spectrometer. Merriam-Webster's Collegiate Dictionary, 10th Edition (1999) defines spectrometry as the adjective form of spectrometer (see page 1129), and the second definition states:

any of various analytical instruments in which an emission (as of particles or radiation) is dispersed according to some property (as mass or energy) of the emission and the amount of the dispersion is measured <nuclear magnetic resonance>

Thus, one of skill in the art at the time of application would recognize that the term "spectrometry" includes more than just mass spectrometry, as alleged by the Examiner. The term encompasses the use of various analytical instruments as defined above, and the Collegiate Dictionary provides as an example nuclear magnetic resonance. Thus, the subject matter of claim 2 is patently distinct from the subject matter of claim 3. Claim 2 encompasses, for example, a spectrometry data set generated by an NMR, a mass spectrometer, or any of various analytical instruments in which an emission (as of particles or radiation) is dispersed according to some property (as mass or energy) of the emission and the amount of the dispersion is measured. Claim 3 is directed to the method of claim 1 where the data set is generated by a mass spectrometer. Therefore, claim 2 is not a substantial duplicate of claim 3. Applicant respectfully requests that the objection be withdrawn.

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In view of the remarks herein, reconsideration and allowance of the application are respectfully requested.

Respectfully submitted,
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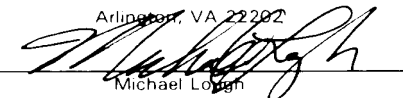
Applicant: Yip
Serial No.: 09/663,968
Confirmation No.: 4499
Filed: September 19, 2000
For: *METHOD AND DEVICE FOR
IDENTIFYING BIOLOGICAL
SAMPLES*
Art Unit: 1631
Examiner: Mahatan, C.

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ATTACHMENT TO THE AMENDMENT SHOWING
MARKED UP PARAGRAPHS AND CLAIMS (37 CFR §1.121)

Please amend claims as follows (insertions are underlined, deletions are [bracketed]):

1. (2x Amended) A method for identifying a biological sample, comprising:
 - generating a data set comprising compositional data [indicative of the composition of] regarding the biological sample;
 - denoising the data set to generate denoised data;
 - correcting [deleting] the baseline from the denoised data to generate an intermediate data set;
 - defining putative peaks for the biological sample;
 - using the putative peaks to remove residual baseline effects, generating [generate] a residual baseline;
 - removing the residual baseline from the intermediate data set to generate a corrected data set;
 - locating[, responsive to removing the residual baseline,] a probable peak in the corrected data set; and
 - identifying, using the located probable peak, the biological sample.

lower stages.

13. (2x Amended) The method according to claim 5, further including generating a sparse data set comprising [indicative of] the denoised data.

19. (2x Amended) The method according to claim 1, further including the step of compressing the intermediate data set subsequent to removing the residual baseline, comprising

a) generating an x-y array of coefficients from the intermediate data set;

b) determining a data starting point and a data maximum;

c) generating intermediate compressed data values for each data point; and

d) calculating compressed data values to form a compressed data set; [the intermediate data set having a plurality of data values associated with respective addresses]

wherein the compressed data set is used in the locating step.

20. (2x Amended) The method according to claim 19, wherein the[a] intermediate compressed data value is a real number that includes a whole number portion representing the non-zero wavelet coefficient of each of the denoised data. [the difference between two addresses].

21. (2x Amended) The method according to claim 19, wherein the[a] intermediate compressed data value is a real number that includes a decimal portion representing the quotient of the value of the wavelet coefficient of the denoised data divided by the maximum wavelet coefficient value. [the difference between a maximum value of all the data values and a value at a particular address.]

38. (2x Amended) A system for identifying a biological sample, the system comprising:

an instrument receiving the biological sample and generating a data set

computer communicating to the instrument and configured to receive

the generated data set, the computer performing the method of:

- denoising the data set to generate denoised data;
- correcting [deleting] the baseline from the denoised data to generate an intermediate data set;
- defining putative peaks for the biological sample;
- using the putative peaks to remove residual baseline effects, generating [generate] a residual baseline;
- removing the residual baseline from the intermediate data set to generate a corrected data set;
- locating[, responsive to removing the residual baseline,] a probable peak in the corrected data set; and
- identifying, using the located probable peak, the biological sample.

40. (Amended) A machine readable program operating on a computing device, the computing device being configured to receive a data set indicating composition of a biological sample, the program implement the steps of:

- denoising the data set to generate denoised data;
- correcting [deleting] the baseline from the denoised data to generate an intermediate data set;
- defining putative peaks for the biological sample;
- using the putative peaks to remove residual baseline effects, generating [generate] a residual baseline;
- removing the residual baseline from the intermediate data set to generate a corrected data set;
- locating[, responsive to removing the residual baseline,] a probable peak in the corrected data set; and
- identifying, using the located probable peak, the biological sample.

41. (Amended) A system for identifying a component of a DNA

- mass spectrometer receiving the DNA sample and generating a

data set indicative of the composition of the DNA sample;

a computing device configured to receive the data set, the computing device implementing the method comprising:

denoising the data set using wavelet transformation to generate denoised data;

correcting [removing sufficiently] the baseline from the denoised data to generate a corrected data set, the corrected data set having putative peaks

using the putative peaks to remove residual baseline effects; locating a probable peak in the corrected data set; and identifying, using the located probable peak, a component in the composition of the DNA sample.

42. (Amended) The system according to claim 41, where the method further includes using a statistical methodology to determine a probability [if] that the located probable peak is an actual peak.

43. (Amended) The system according to claim 42[41], where the method further includes determining a confidence based on a the probability, wherein

the method calls the component of the DNA sample when [whether] the confidence [probability of the actual peak existing] is sufficiently high; and [probability to call the component of the DNA sample, and if the probability is not sufficiently high, then] the method does not call the component when the confidence is not sufficiently high.

44. (Amended) The system according to claim 42[43], where the [percentage of correctly called components]probability is about 100 percent.

45. (Amended) A system for identifying a component in a biological sample, comprising:

indicative of the component in the biological sample

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MARKED-UP CLAIMS

a computing device receiving the data set and performing the steps of:

generating corrected data by processing the data set to remove noise due to system and chemical reaction characteristics, the corrected data set having putative peak areas;

using the putative peaks to remove residual baseline effects;

defining the position of expected peaks using known possible peak areas from the biological sample;

shifting the corrected data set to more closely align the putative peaks to the expected peaks;

calculating the probability that the putative peaks in the shifted data set are actual peaks; and

calling the composition of the biological sample responsive to the calculated probability to thereby identify a component in the sample.